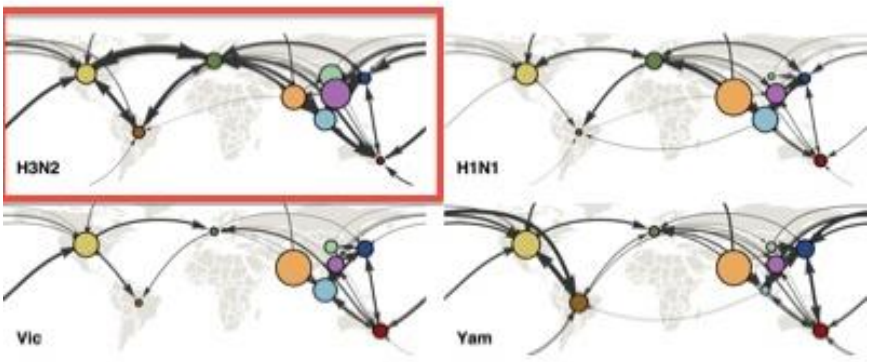
The around-the-world journey of flu

Aug. 17, 2015

L Pattacini



Graphic illustrating estimated path and rate of virus migration for four strains of influenza: H3N2, H1N1, Vic and Yam.

Image provided by Dr. Trevor Bedford.

The flu season can seem so far away during hot and sunny summer days, and most of us do not think about next year's flu. For scientists in charge of producing influenza vaccines, however, there is no time to rest. In fact, summer in the northern hemisphere means flu season in the southern. Furthermore, every year the World Health Organization recommends which strains should be included in next season's vaccine. As several different viruses circulate at the same time, the seasonal vaccine includes two influenza A viruses, H3N2 and H1N1 (where H indicates the subtype of haemagglutinin and N the subtype of neuraminidase, two proteins expressed on the viral surface) and two influenza B viruses. While the global circulation pattern of the H3N2 virus has been partially characterized previously, the migration patterns of the other viruses are not fully known.

All this complexity, together with the need of timely production of effective vaccines, calls for year-long action. "Influenza circulation patterns suggest that H3N2 viruses, in particular, emerge from India, China and Southeast Asia. Focusing surveillance on these areas will help to catch new antigenic variants early. Also, when confronted with a choice in circulating lineages, our work suggests that, other factors being equal, an E-SE Asian lineage will more likely spread to the rest of the world. Both these perspectives can inform vaccine strain selection", explained Dr. Trevor Bedford from the Vaccine and Infectious Disease Division at Fred Hutch. To understand the 'travel itinerary' of influenza, Dr. Bedford and his collaborators compared the global circulation patterns of haemagglutinin genes for two influenza A viruses (H2N3 and H1N1) and two influenza B viruses,

(B/Victoria/2/1987-like [Vic] and B/Yamagata/16/1988-like [Yam]). Findings from these efforts were reported in a paper published in the July issue of Nature.

Similarly to H3N2, viruses H1N1, Vic, and Yam originate in China, Southeast Asia and India. Their global circulation patterns, however, differ substantially from H3N2 viruses. In the case of H1N1, three co-circulating genetic lineages started segregating in 2004-2005 from one common strain, and circulated in Southeast Asia, China and India, until this last lineage eventually dominated and spread worldwide. Vic and Yam also revealed a different pattern, with lineages frequently seeding outside East and Southeast Asia. Furthermore, H3N2 viruses move between regions more frequently than the other analyzed viruses.

Other differences between these strains can lead to differential immune response. Slower antigenic evolution of H1N1 and the B viruses allows a greater fraction of adults to develop an immune response against them, while children are more sensitive and their infection rate is higher. Conversely, the fast paced H3N2 influenza is more likely to infect adults. The reason H3N2 is hypothesized to maintain its fast pace of transmission is that adults are more likely to travel around the world by airplane and to carry around with them the flu that they contracted in another country. Has that ever happened to you? I did bring back to Seattle a flu that I got in Italy when I was there for my Christmas vacations. From then on, I have never forgotten again to vaccinate. Will other adults make the same choice? Will influenza patterns change again as more adults decide to vaccinate?

To know, we will have to wait for Dr. Bedford to solve this enigma!

Bedford T, Riley S, Barr IG, Broor S, Chadha M, Cox NJ, Daniels RS, Gunasekaran CP, Hurt AC, Kelso A, Klimov A, Lewis NS, Li X, McCauley JW, Odagiri T, Potdar V, Rambaut A, Shu Y, Skepner E, Smith DJ, Suchard MA, Tashiro M, Wang D, Xu X, Lemey P, Russell CA. 2015. Global circulation patterns of seasonal influenza viruses vary with antigenic drift. Nature. 523: 217-220.

The research was supported by grants from the NIH and other US and international funding agencies.

Supplementary information: Video.